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## Introducing the genetic variability in crop models by combining phenotyping with modelling

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Linking crop models with genetic analyses potentially allow prediction of the comparative advantages of genotypes under environmental scenarios with water or temperature stresses (Parent & Tardieu, 2014, Technow et al., 2015). Hence, we are working on the integration of genotype-dependent parameters measured in a phenotyping platform in a crop model. The first step, presented here, involves the adaptation of the existing module of leaf development to incorporate genotypic variability in its formalisms and parameters.

We have worked on an existing leaf expansion model developed in APSIM, which applied to virtual genotypes differing only on maximum leaf growth rate and its sensitivity to soil water deficit and vapour pressure deficit (Chenu et al., 2008, 2009). We have extended it to represent real genotypes differing in maximum number of leaves, timing of leaf initiation, appearance and duration of leaf expansion, shape of leaves (length vs. width) and sensitivity to water deficit and evaporative demand. First, parameters have been extracted from platform raw data. For example:

The phyllochron was estimated in 250 genotypes in the platform. It was highly heritable in a series of experiments (Fig. 1A, E. Millet and C. Welcker) and very close to those measured in the field in few genotypes.

Parameters representing the timings of development of every leaf have been considered as dependent on final leaf number only. They have been estimated in a series of hybrids and considered as valid for any genotype with the same leaf number.

Parameters describing the sensitivity of leaf growth to water deficit (Fig 1B, S. Alvarez Prado) and evaporative demand were extracted from platform experiments.

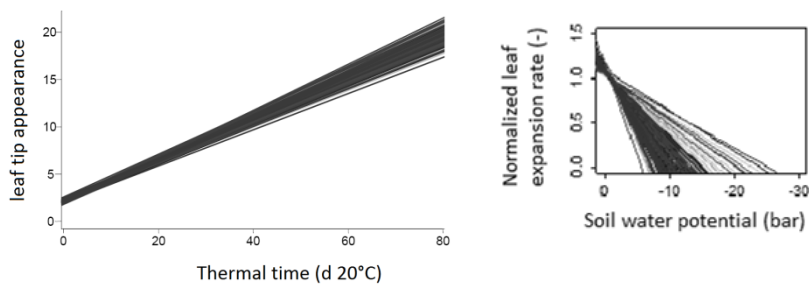


Figure 1. A. Range of variation of the phyllochron. B. Range of variation of sensitivity of leaf expansion to water deficit. Both for 250 genotypes measured in the PhenoArch Platform (INRA-LEPSE).

We paid special attention to minimize the number of parameters in formalisms with only easily measurable parameters (for leaf/plant development, leaf growth, and leaf architecture). The resulting model uses four genotypic parameters to simulate leaf development, namely: final leaf number, phyllochron, the slope of the progression of leaf ligulation with thermal time and thermal time at emergence. This is in addition to (i) maximum leaf elongation rate (assumed to vary between successive leaves in a way that only depends on final leaf number), (ii) sensitivities to evaporative demand and soil water potential, assumed to be common to all leaves, (iii) leaf width and its relationship with light.

We are currently testing the adapted model in relation with a network of 30 experiments in the field to investigate its capacity of simulating genotype by environment interaction.

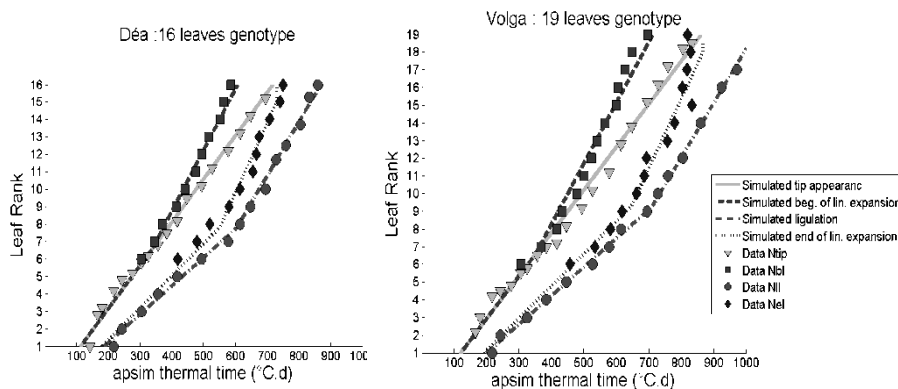


Figure 2. Simulated and measured data for 16 and 19 leaves genotypes for leaf appearance, beginning of linear elongation, end of linear elongation and ligulation.

## Conclusion

This work is a "proof of concept" showing that it is feasible to incorporate the genetic variability of hundred of genotypes in a crop model *via* vectors of measured parameters. In the long term, genomic prediction will allow estimations of genotypic parameters of crop models (Technow et al 2015). Combined with multi-environment simulations, this can help defining the suitability of any genotype, traits or allele in a large range of environmental scenarios.

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## References

- Chenu, K., SC. Chapman, GL. Hammer et al., (2008). *Plant, Cell and Environment*, 31: 378-391
- Chenu, K., SC. Chapman, F. Tardieu et al., (2009). *Genetics*, 183 : 1507-1523
- Parent, B. and F. Tardieu (2014). *Journal of experimental Botany*, 65: 6179-6189
- Technow F, Messina CD, Totir LR, Cooper M (2015) *Plos One*, 10